

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5 (i) APPLICANT: Melton, Douglas A.  
Hemmati-Brivanlou, Ali

10 (ii) TITLE OF INVENTION: Method of Inducing and Maintaining  
Neuronal Cells

(iii) NUMBER OF SEQUENCES: 2

15 (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: LAHIVE & COCKFIELD  
(B) STREET: 60 State Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
20 (F) ZIP: 02109

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: ASCII(TEXT)

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
30 (B) FILING DATE: 09-MAR-1995  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Vincent, Matthew P.  
35 (B) REGISTRATION NUMBER: 36,709  
(C) REFERENCE/DOCKET NUMBER: HUI-009

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (617) 227-7400  
40 (B) TELEFAX: (617) 227-5941

## (2) INFORMATION FOR SEQ ID NO:1:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
55 (A) NAME/KEY: CDS  
(B) LOCATION: 108..1067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60 GCGGCCGCCC CCCCCCGT CATTCAATAG AGTCCGGACT TGTGCCTGGT CCATTATCCC 60

ATCTCTCTCC ACTTGAGACT CTGCTCGTCC CACTCCCAGC ACTGAGG ATG TTA AAT 116  
Met Leu Asn  
65 1

	GAA AGG ATC CAG CCG GGC ATG ATT TTC CTC CTG ACT GTC TCC CTG TGC	164
	Glu Arg Ile Gln Pro Gly Met Ile Phe Leu Leu Thr Val Ser Leu Cys	
	5	
5	CAT TTC ATG GAA TAT CGC GCA GTC CAA GCT GGG AAT TGC TGG CTG CAG	212
	His Phe Met Glu Tyr Arg Ala Val Gln Ala Gly Asn Cys Trp Leu Gln	
	20 25 30 35	
10	CAG TCG AAG AAT GGC CGA TGT CAG GTT CTG TAC AGG ACA GAA CTG AGC	260
	Gln Ser Lys Asn Gly Arg Cys Gln Val Leu Tyr Arg Thr Glu Leu Ser	
	40 45 50	
15	AAA GAG GAA TGC TGC AAG ACT GGC AGA CTG GGC ACC TCA TGG ACA GAA	308
	Lys Glu Glu Cys Lys Thr Gly Arg Leu Gly Thr Ser Trp Thr Glu	
	55 60 65	
20	GAA GAT GTA CCC AAC AGC ACC CTC TTC AAA TGG ATG ATA TTT CAT GGA	356
	Glu Asp Val Pro Asn Ser Thr Leu Phe Lys Trp Met Ile Phe His Gly	
	70 75 80	
25	GGG GCC CCA CAT TGC ATC CCC TGC AAA GAA ACA TGT GAG AAC GTA GAC	404
	Gly Ala Pro His Cys Ile Pro Cys Lys Glu Thr Cys Glu Asn Val Asp	
	85 90 95	
30	TGT GGC CCT GGG AAG AAA TGT AAA ATG AAC AAG AAG AAC AAG CCG AGG	452
	Cys Gly Pro Gly Lys Lys Cys Lys Met Asn Lys Lys Asn Lys Pro Arg	
	100 105 110 115	
35	TGT GTC TGC GCT CCG GAT TGT TCC AAC ATT ACT TGG AAA GGT TCA GTG	500
	Cys Val Cys Ala Pro Asp Cys Ser Asn Ile Thr Trp Lys Gly Ser Val	
	120 125 130	
40	TGC GGA ATT GAT GGC AAA ACC TAT AAG GAT GAG TGC GCT TTG CTC AAA	548
	Cys Gly Ile Asp Gly Lys Thr Tyr Lys Asp Glu Cys Ala Leu Leu Lys	
	135 140 145	
45	GCC AAA TGT AAA GGG GTC CCG GAG CTG GAT GTG CAG TAC CAA GGA AAA	596
	Ala Lys Cys Lys Gly Val Pro Glu Leu Asp Val Gln Tyr Gln Gly Lys	
	150 155 160	
50	TGC AAA AAG ACT TGC AGG GAC GTG CTG TGT CCA GGG AGC TCC TCG TGT	644
	Cys Lys Lys Thr Cys Arg Asp Val Leu Cys Pro Gly Ser Ser Ser Cys	
	165 170 175	
55	GTG GTG GAT CAG ACC AAT AAC GCC TAC TGT GTG ACA TGT AAT CGG ATT	692
	Val Val Asp Gln Thr Asn Asn Ala Tyr Cys Val Thr Cys Asn Arg Ile	
	180 185 190 195	
60	TGC CCG GAG CCT ACC TCC CCT GAC CAA TAT CTG TGT GGG AAT GAT GGA	740
	Cys Pro Glu Pro Thr Ser Pro Asp Gln Tyr Leu Cys Gly Asn Asp Gly	
	200 205 210	
65	ATA ACC TAT GGA AGT GCG TGC CAC CTG AGG AAG GCT ACC TGC CTG CTG	788
	Ile Thr Tyr Gly Ser Ala Cys His Leu Arg Lys Ala Thr Cys Leu Leu	
	215 220 225	
70	GGC AGA TCC ATT GGA TTA GCC TAC GAG GGG AAA TGC ATA AAA GCC AAG	836
	Gly Arg Ser Ile Gly Leu Ala Tyr Glu Gly Lys Cys Ile Lys Ala Lys	
	230 235 240	
75	TCT TGT GAA GAT ATT CAG TGC AGC GCT GGA AAG AAA TGC CTG TGG GAC	884
	Ser Cys Glu Asp Ile Gln Cys Ser Ala Gly Lys Lys Cys Leu Trp Asp	
	245 250 255	
80	AGT AGA GTG GGT AGA GGT CGC TGT GCG CTG TGC GAT GAT CTG TGC GGA	932
	Ser Arg Val Gly Arg Gly Arg Cys Ala Leu Cys Asp Asp Leu Cys Gly	

	260		265			270		275	
	GAG AGC AAG TCA GAC GAT ACA GTG TGC GCC AGC GAC AAC ACG ACT TAC								980
5	Glu Ser Lys Ser Asp Asp Thr Val Cys Ala Ser Asp Asn Thr Thr Tyr		280			285		290	
	CCG AGC GAG TGC GCC ATG AAA CAG GCA GCC TGC TCC ACG GGG ATT CTT								1028
10	Pro Ser Glu Cys Ala Met Lys Gln Ala Ala Cys Ser Thr Gly Ile Leu		295			300		305	
	TTG GAA GTG AAA CAC AGT GGA TCT TGC AAC TGT AAG TGAATTACCG								1074
	Leu Glu Val Lys His Ser Gly Ser Cys Asn Cys Lys		310			315		320	
15	CAACGCAGAG TAAGATTTCT AAAGGCAACC CCTCGTAAT GAAGACTTTA AAGCAGCAAA								1134
	ATACTTTTTTT TTTTTTTTTT TCCTTTTTTTT CTAAGGGAAT TCAG								1178
20	(2) INFORMATION FOR SEQ ID NO:2:								
	(i) SEQUENCE CHARACTERISTICS:								
	(A) LENGTH: 319 amino acids								
	(B) TYPE: amino acid								
25	(D) TOPOLOGY: linear								
	(ii) MOLECULE TYPE: protein								
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:								
30	Met Leu Asn Glu Arg Ile Gln Pro Gly Met Ile Phe Leu Leu Thr Val								
	1		5			10		15	
35	Ser Leu Cys His Phe Met Glu Tyr Arg Ala Val Gln Ala Gly Asn Cys		20		25		30		
	Trp Leu Gln Gln Ser Lys Asn Gly Arg Cys Gln Val Leu Tyr Arg Thr		35		40		45		
40	Glu Leu Ser Lys Glu Glu Cys Cys Lys Thr Gly Arg Leu Gly Thr Ser		50		55		60		
	Trp Thr Glu Glu Asp Val Pro Asn Ser Thr Leu Phe Lys Trp Met Ile		65		70		75		80
45	Phe His Gly Gly Ala Pro His Cys Ile Pro Cys Lys Glu Thr Cys Glu		85		90		95		
50	Asn Val Asp Cys Gly Pro Gly Lys Lys Cys Lys Met Asn Lys Lys Asn		100		105		110		
	Lys Pro Arg Cys Val Cys Ala Pro Asp Cys Ser Asn Ile Thr Trp Lys		115		120		125		
55	Gly Ser Val Cys Gly Ile Asp Gly Lys Thr Tyr Lys Asp Glu Cys Ala		130		135		140		
	Leu Leu Lys Ala Lys Cys Lys Gly Val Pro Glu Leu Asp Val Gln Tyr		145		150		155		160
60	Gln Gly Lys Cys Lys Lys Thr Cys Arg Asp Val Leu Cys Pro Gly Ser		165		170		175		
65	Ser Ser Cys Val Val Asp Gln Thr Asn Asn Ala Tyr Cys Val Thr Cys		180		185		190		

	Asn	Arg	Ile	Cys	Pro	Glu	Pro	Thr	Ser	Pro	Asp	Gln	Tyr	Leu	Cys	Gly	
			195					200					205				
5	Asn	Asp	Gly	Ile	Thr	Tyr	Gly	Ser	Ala	Cys	His	Leu	Arg	Lys	Ala	Thr	
		210					215					220					
	Cys	Leu	Leu	Gly	Arg	Ser	Ile	Gly	Leu	Ala	Tyr	Glu	Gly	Lys	Cys	Ile	
	225					230					235					240	
10	Lys	Ala	Lys	Ser	Cys	Glu	Asp	Ile	Gln	Cys	Ser	Ala	Gly	Lys	Lys	Cys	
					245					250					255		
	Leu	Trp	Asp	Ser	Arg	Val	Gly	Arg	Gly	Arg	Cys	Ala	Leu	Cys	Asp	Asp	
				260					265					270			
15	Leu	Cys	Gly	Glu	Ser	Lys	Ser	Asp	Asp	Thr	Val	Cys	Ala	Ser	Asp	Asn	
			275					280					285				
	Thr	Thr	Tyr	Pro	Ser	Glu	Cys	Ala	Met	Lys	Gln	Ala	Ala	Cys	Ser	Thr	
20							295					300					
	Gly	Ile	Leu	Leu	Glu	Val	Lys	His	Ser	Gly	Ser	Cys	Asn	Cys	Lys		
	305					310					315						